

## SEQUENCE LISTING

<110> Goodwin, Raymond G  
Din, Wanwan S.

<120> METHODS OF USE OF THE TACI/TACI-L INTERACTION

<130> 2519

<140> 09/302,863

<141> 1999-04-30

<160> 5

<170> PatentIn Ver. 2.0

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<212> DNA

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<221> CDS

<222> (14)..(892)

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agc cgt gtg gac cag gag gag cgc ttc cca cag ggc ctg tgg acg ggg      97
Ser Arg Val Asp Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly
      15              20              25

gtg gct atg aga tcc tgc ccc gaa gag cag tac tgg gat cct ctg ctg      145
Val Ala Met Arg Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu
      30              35              40

ggg acc tgc atg tcc tgc aaa acc att tgc aac cat cag agc cag cgc      193
Gly Thr Cys Met Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg
      45              50              55              60

acc tgt gca gcc ttc tgc agg tca ctc agc tgc cgc aag gag caa ggc      241
Thr Cys Ala Ala Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly
          65              70              75

aag ttc tat gac cat ctc ctg agg gac tgc atc agc tgt gcc tcc atc      289
Lys Phe Tyr Asp His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile
          80              85              90

tgt gga cag cac cct aag caa tgt gca tac ttc tgt gag aac aag ctc      337
Cys Gly Gln His Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu
          95              100              105

agg agc cca gtg aac ctt cca cca gag ctc agg aga cag cgg agt gga      385
Arg Ser Pro Val Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly
      110              115              120

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gaa gtt gaa aac aat tca gac aac tct gga agg tac caa gga ttg gag 433  
Glu Val Glu Asn Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu  
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cac aga ggc tca gaa gca agt cca gct ctc ccg ggg ctg aag ctg agt 481  
 His Arg Gly Ser Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser  
 145 150 155

gca gat cag gtg gcc ctg gtc tac agc acg ctg ggg ctc tgc ctg tgt 529  
Ala Asp Gln Val Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys  
160 165 170

gcc gtc ctc tgc tgc ttc ctg gtg gcg gtg gcc tgc ttc ctc aag aag 577  
Ala Val Leu Cys Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys  
175 180 185

agg ggg gat ccc tgc tcc tgc cag ccc cgc tca agg ccc cgt caa agt 625  
Arg Gly Asp Pro Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser  
190 195 200

cgc gcc aag tct tcc cag gat cac gcg atg gaa gcc ggc agc cct gtg 673  
Pro Ala Lys Ser Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val  
205 210 215 220

agc aca tcc ccc gag cca gtg gag acc tgc agc ttc tgc ttc cct gag 721  
 Ser Thr Ser Pro Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu  
 225 230 235

tgc agg gcg ccc acg cag gag agc gca gtc acg cct ggg acc ccc gac 769  
 Cys Arg Ala Pro Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp  
 240 245 250

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ccc act tgt gct gga agg tgg ggg tgc cac acc agg acc aca gtc ctg      817
Pro Thr Cys Ala Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu
      255                      260                      265

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cag cct tgc cca cac atc cca gac agt ggc ctt ggc att gtg tgt gtg 865  
Gln Pro Cys Pro His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val  
270 275 280

cct gcc cag gag ggg ggc cca ggt gca taaatggggg tcaggagggg 912  
Pro Ala Gln Glu Gly Gly Pro Gly Ala  
285 290

aaaggaggag ggagagagat ggagaggagg ggagagagaa agagagggtgg ggagagggga 972

gagagatatg aggagagaga gacagaggag gcagaaaggg agagaaacag aggagacaga 1032

gagggagaga gagacagagg gagagagaga cagaggggaa gagaggcaga gagggaaaga 1092

ggcagagaag gaaagagaca ggcagagaag gagagaggca gagagggaga gaggcagaga 1152

gggagagagg cagagagaca gagagggaga gagggacaga gagagataga gcaggagggtc 1212

ggggcactct gagtcccagt tcccagtgca gctgtaggtc gtcatcacct aaccacacgt 1272

gcaataaagt cctcgtgcct gctgctcaca gcccccgaga gccctctctc ctggagaata 1332

aaacctttgg cagctgccct tcctcaaaaa aaaaaaaaaa aaaaa 1377

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Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg Ser Arg Val Asp  
1 5 10 15

Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met  
35 40 45

Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp  
65 70 75 80

Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Pro Val  
100 105 110

Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val Glu Asn  
115 120 125

Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg Gly Ser  
130 135 140

Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp Gln Val  
145                   150                   155                   160

Ala Leu Val Tyr Ser Thr/Leu Gly Leu Cys Leu Cys Ala Val Leu Cys  
165 170 175

Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys Arg Gly Asp Pro  
180 185 190

Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser Pro Ala Lys Ser  
195 200 205

Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val Ser Thr Ser Pro  
210 215 220

Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu Cys Arg Ala Pro  
225 230 235 240

Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp Pro Thr Cys Ala  
245 250 255

Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu Gln Pro Cys Pro  
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Met Asp Asp Ser Thr Glu Arg Glu Gln Ser Arg Leu Thr Ser Cys Leu  
1 5 10 15  
  
aag aaa aga gaa gaa atg aaa ctg aag gag tgt gtt tcc atc ctc cca 153  
Lys Lys Arg Glu Glu Met Lys Leu Lys Glu Cys Val Ser Ile Leu Pro  
20 25 30  
  
cgg aag gaa agc ccc tct gtc cga tcc tcc aaa gac gga aag ctg ctg 201  
Arg Lys Glu Ser Pro Ser Val Arg Ser Ser Lys Asp Gly Lys Leu Leu  
35 40 45  
  
gct gca acc ttg ctg ctg gca ctg ctg tct tgc tgc ctc acg gtg gtg 249  
Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Cys Cys Leu Thr Val Val  
50 55 60  
  
tct ttc tac cag gtg gcc gcc ctg caa ggg gac ctg gcc agc ctc cgg 297  
Ser Phe Tyr Gln Val Ala Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg  
65 70 75 80  
  
gca gag ctg cag ggc cac cac gcg gag aag ctg cca gca gga gca gga 345  
Ala Glu Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Gly Ala Gly  
85 90 95  
  
gcc ccc aag gcc ggc ctg gag gaa gct cca gct gtc acc gcg gga ctg 393  
Ala Pro Lys Ala Gly Leu Glu Glu Ala Pro Ala Val Thr Ala Gly Leu  
100 105 110  
  
aaa atc ttt gaa cca cca gct cca gga gaa ggc aac tcc agt cag aac 441  
Lys Ile Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn  
115 120 125  
  
agc aga aat aag cgt gcc gtt cag ggt cca gaa gaa aca gtc act caa 489  
Ser Arg Asn Lys Arg Ala Val Gln Gly Pro Glu Glu Thr Val Thr Gln  
130 135 140  
  
gac tgc ttg caa ctg att gca gac agt gaa aca cca act ata caa aaa 537  
Asp Cys Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys  
145 150 155 160  
  
gga tct tac aca ttt gtt cca tgg ctt ctc agc ttt aaa agg gga agt 585  
Gly Ser Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser  
165 170 175

gcc cta gaa gaa aaa gag aat aaa ata ttg gtc aaa gaa act ggt tac 633  
Ala Leu Glu Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr  
180 185 190

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ttt ttt ata tat ggt cag gtt tta tat act gat aag acc tac gcc atg    681
Phe Phe Ile Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met
      195                      200                      205

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gga cat cta att cag agg aag aag gtc cat gtc ttt ggg gat gaa ttg 729  
Gly His Leu Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu  
210 215 220

agt ctg gtg act ttg ttt cga tgt att caa aat atg cct gaa aca cta 777  
 Ser Leu Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Glu Thr Leu  
 225 230 235 240

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ccc aat aat tcc tgc tat tca gct ggc att gca aaa ctg gaa gaa gga      825
Pro Asn Asn Ser  Cys  Tyr  Ser Ala  Gly Ile Ala Lys Leu Glu Glu Gly
          245                      250                      255

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gat gaa ctc caa ctt gca ata cca aga gaa aat gca caa ata tca ctg 873  
Asp Glu Leu Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Leu  
260 265 270

gat gga gat gtc aca ttt ttt ggt gca ttg aaa ctg ctg tgacctactt 922  
Asp Gly Asp Val Thr Phe Phe Gly Ala Leu Lys Leu Leu  
275 280 285

acaccatgtc tgtagctatt ttcttccctt tctctgtacc tctaagaaga aagaatctaa 982

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Arg Lys Glu Ser Pro Ser Val Arg Ser Ser Lys Asp Gly Lys Leu Leu  
35 40 45

Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Cys Cys Leu Thr Val Val  
50 55 60

Ser Phe Tyr Gln Val Ala Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg  
65 70 75 80

Ala Glu Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Gly Ala Gly  
85 90 95



Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys Gly Ser Tyr Thr Phe Val  
100 105 110

Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser Ala Leu Glu Glu Lys Glu  
115 120 125

Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr Phe Phe Ile Tyr Gly Gln  
130 135 140

Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met Gly His Leu Ile Gln Arg  
145 150 155 160

Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu Val Thr Leu Phe  
165 170 175

Arg Ile Cys Ile Gln Asn Met Pro Glu Thr Leu Pro Asn Asn Ser Cys  
180 185 190

Tyr Ser Ala Gly Ile Ala Lys Leu Glu Glu Gly Asp Glu Leu Gln Leu  
195 200 205

Ala Thr Pro Arg Glu Asn Ala Gln Ile Ser Leu Asp Gly Asp Val Thr  
210 215 220

Phe Phe Gly Ala Leu Lys Leu Leu  
225 230

100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230